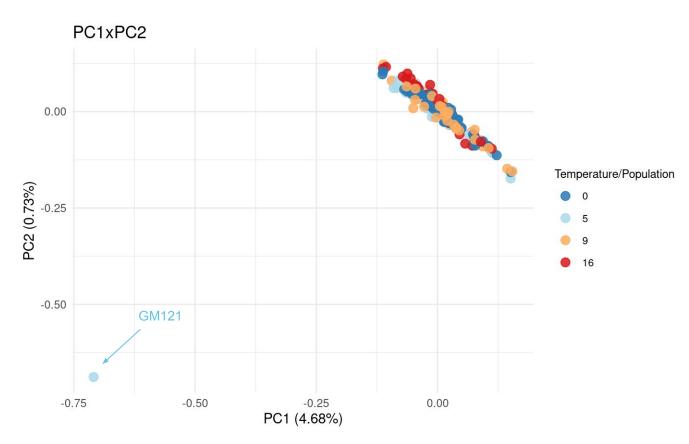# Juvenile P. cod temperature experiment

Genetic analysis using lcWGS
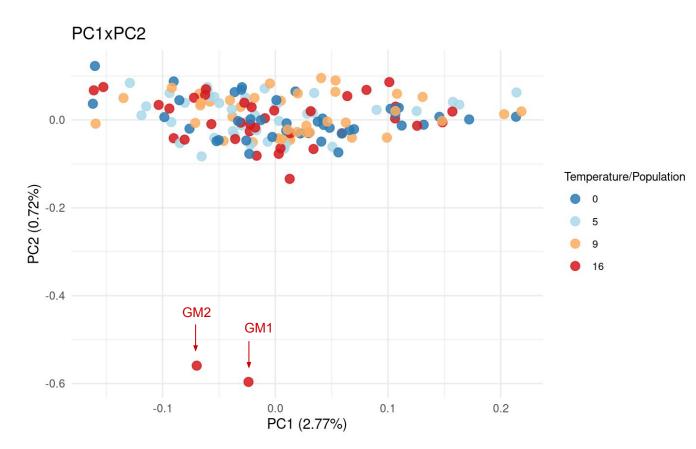
Method:

- low coverage Whole Genome Sequencing (lcWGS)

- Data analyzed using AFSC-developed pipeline (Laura Timm, Sara Schaal), https://github.com/AFSC-Genetics/lcWGS-pipeline

- Covariate matrices from lcWGS pipeline into PCA
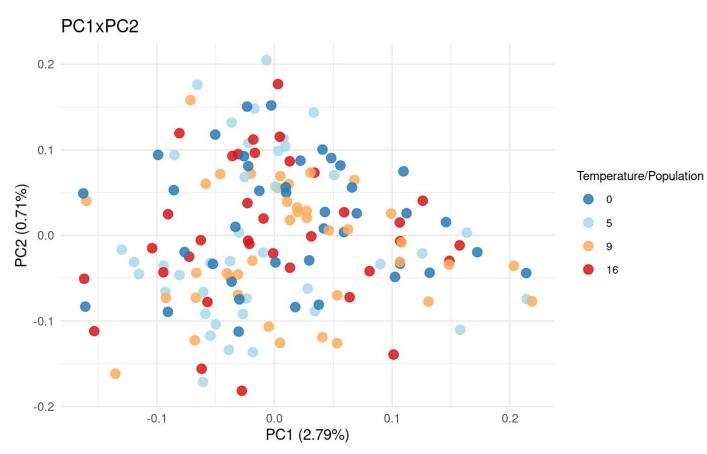
- PCAs to assess population structure (or lack thereof)

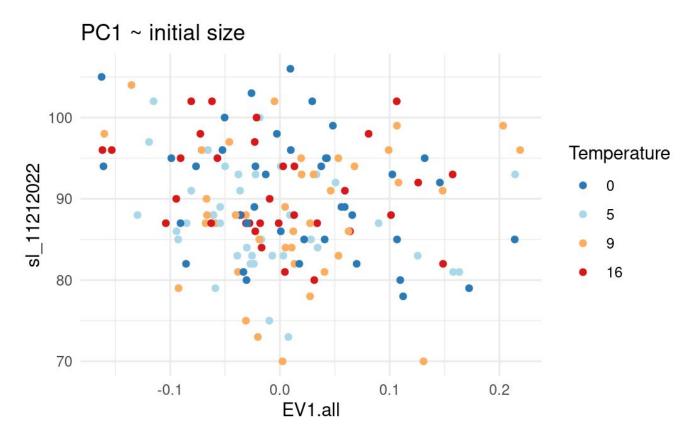# PC1 x PC 2, ALL experimental fish
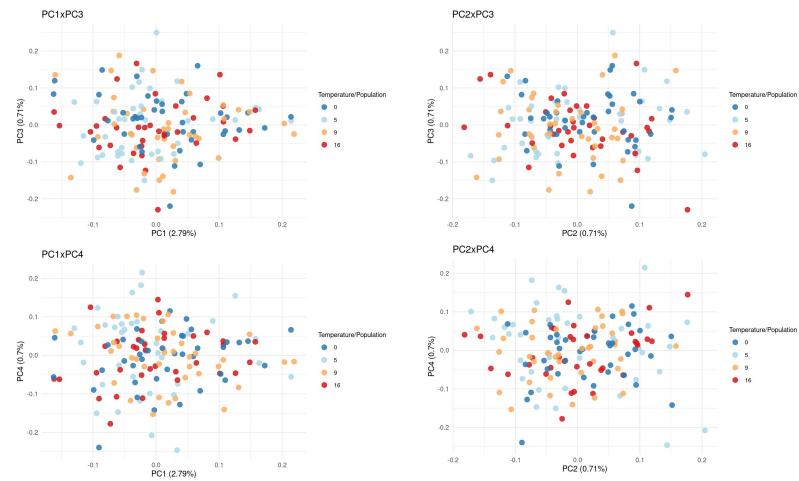
PC1 x PC 2, Outlier sample GM121 removed
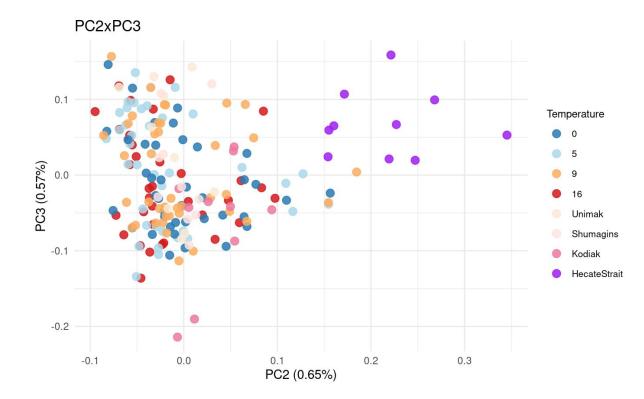
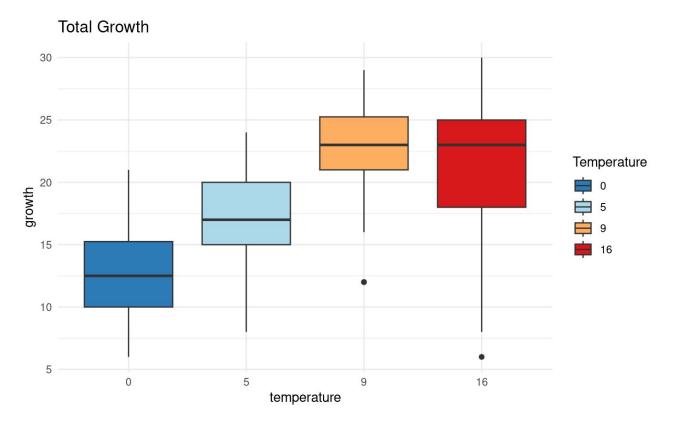# PC1 x PC 2, all outliers removed (GM121, GM1, and GM2)

PC1 ~ initial size

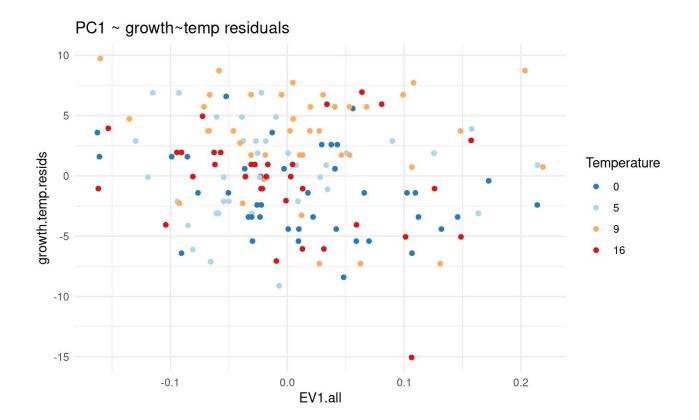# Other axes, our experimental fish (outliers removed)

PC2 x PC3, experimental + reference fish
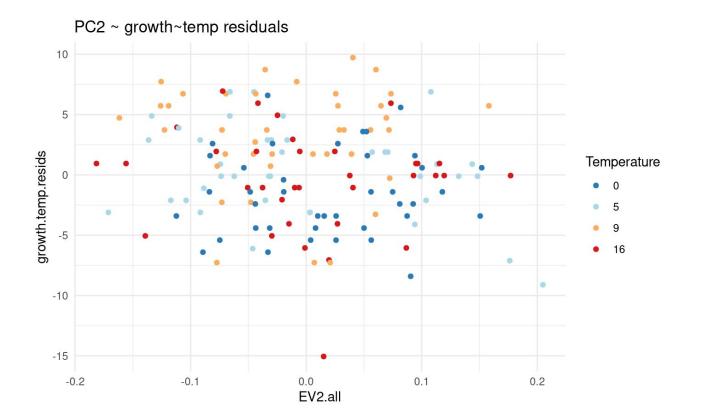## *PC2 indicates fish from Kodiak/Unimak/Shumagins pop*
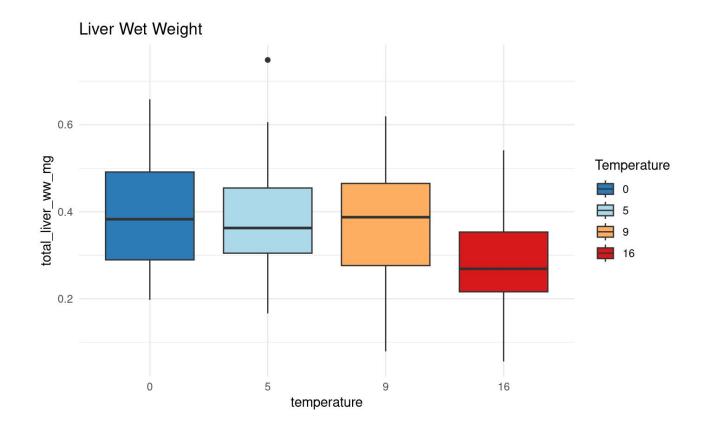

PC2xPC3

Growth rate varied among most treatments (except 9vs16)

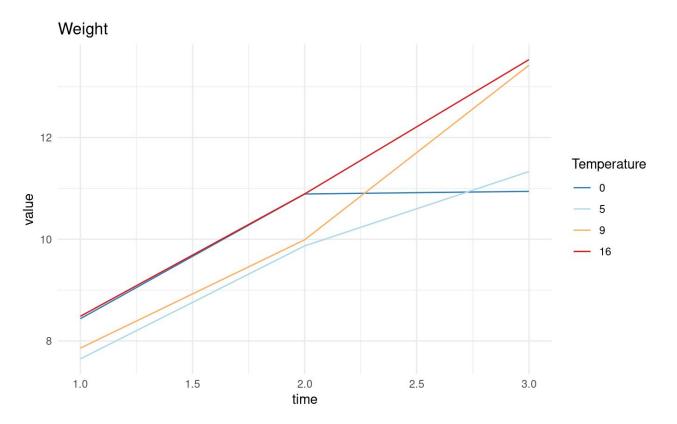# PC1 scores ~ residuals from growth~temp linear model

PC1 scores ~ residuals from growth~temp linear model

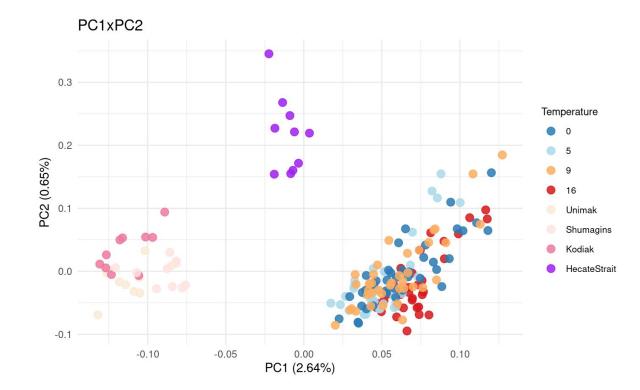PC2 ~ growth~temp residuals

Livers smaller in 16°C group

Wet weight over time

Additional figures

PC1 x PC 2, experimental + reference fish
strong batch effect along PC1

PC2 x other axes, experimental + reference fish
PC2 indicates fish from Kodiak/Unimak/Shumagins pop